

SEQUENCE LISTING

<110> Meyers, Rachel A.
MacBeth, Kyle J.

<120> 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
USES THEREFOR

<130> 10448-046002

<150> US 09/633,300

<151> 2000-08-08

<150> US 60/200,621

<151> 2000-04-28

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (628)... (1986)

<221> misc_feature

<222> (1)... (2948)

<223> n = A,T,C or G

<400> 1

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gtattttcttc cagggtaaaa agcaaaagaa ttccgggttt ctgtatcctt ttcacttact    180
gttaccctact ttgcctcgtc ttcaccctgt ccaaacaccg gtctccaatt tgcccttcag    240
agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca    300
ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc    360
caaactccaa aaaaaaaccc gaattcagcc tgggttaagtc caagctgaat tccgggtggg    420
ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattagggtc atgcccgtat    480
gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc    540
gtggtgccat ctacattttt gggactcggg aattatgagg tagagggtgga ggcggagccg    600
gatgtcagag gtcttgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt    654
Met Gly Glu Asn Asp Pro Pro Ala Val

```

1

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gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa    702
Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
10                      15                      20                      25

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ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg    750
Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
30                      35                      40

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tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att	798
Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile	
45 50 55	
gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc	846
Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys	
60 65 70	
tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata	894
Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile	
75 80 85	
gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac	942
Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	
90 95 100 105	
cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca	990
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr	
110 115 120	
gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac	1038
Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr	
125 130 135	
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca	1086
Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser	
140 145 150	
gat aac ctc aga gtg agc tcg ctg gag ggg cag ttc cgg gag gag ttt	1134
Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe	
155 160 165	
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac	1182
Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His	
170 175 180 185	
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc	1230
His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr	
190 195 200	
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc	1278
Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile	
205 210 215	
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc	1326
Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser	
220 225 230	
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc	1374
Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro	
235 240 245	
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc	1422
Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro	
250 255 260 265	
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca	1470

Lys	Ser	Trp	Thr	Ile	Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro				
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gcc	cca	tcc	cac	ttg	gtg	gag	aag	att	gtc	tac	cac	agc	aag	tac	aag	1518			
Ala	Pro	Ser	His	Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys				
				285								290							
cca	aag	agg	ctg	ggc	aat	gac	atc	gcc	ctt	atg	aag	ctg	gcc	ggg	cca	1566			
Pro	Lys	Arg	Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro				
				300								305							
ctc	acg	ttc	aat	gaa	atg	atc	cag	cct	gtg	tgc	ctg	ccc	aac	tct	gaa	1614			
Leu	Thr	Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu				
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gag	aac	ttc	ccc	gat	gga	aaa	gtg	tgc	tgg	acg	tca	gga	tgg	ggg	gcc	1662			
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aca	gag	gat	gga	ggg	gac	gcc	tcc	cct	gtc	ctg	aac	cac	gcg	gcc	gtc	1710			
Thr	Glu	Asp	Gly	Gly	Asp	Ala	Ser	Pro	Val	Leu	Asn	His	Ala	Ala	Val				
				350								355							
cct	ttg	att	tcc	aac	aag	atc	tgc	aac	cac	agg	gac	gtg	tac	ggg	ggc	1758			
Pro	Leu	Ile	Ser	Asn	Lys	Ile	Cys	Asn	His	Arg	Asp	Val	Tyr	Gly	Gly				
				365								370							
atc	atc	tcc	ccc	tcc	atg	ctc	tgc	gcg	ggc	tac	ctg	acg	ggg	ggc	gtg	1806			
Ile	Ile	Ser	Pro	Ser	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Thr	Gly	Gly	Val				
				380								385							
gac	agc	tgc	cag	ggg	gac	agc	ggg	ggg	ccc	ctg	gtg	tgt	caa	gag	agg	1854			
Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln	Glu	Arg				
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agg	ctg	tgg	aag	tta	gtg	gga	gcg	acc	agc	ttt	ggc	atc	ggc	tgc	gca	1902			
Arg	Leu	Trp	Lys	Leu	Val	Gly	Ala	Thr	Ser	Phe	Gly	Ile	Gly	Cys	Ala				
				410								415							
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Glu	Val	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Ser	Phe	Leu	Asp				
				430								435							
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Trp	Ile	His	Glu	Gln	Met	Glu	Arg	Asp	Leu	Lys	Thr								
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cgctcctttc	tgatcttcac			taagaacaaa			agaagcagca			acttgcaagg			gcggcctttc			2536			
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<210> 2
<211> 453
<212> PRT
<213> Homo sapiens
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Ala	Asp 35	Ala	Val	Ala	Ala	Gln	Ile 40	Leu	Ser	Leu	Leu	Pro 45	Leu	Lys	Phe	
Phe 50	Pro	Ile	Ile	Val	Ile	Gly 55	Ile	Ile	Ala	Leu	Ile 60	Leu	Ala	Leu	Ala	
Ile 65	Gly	Leu	Gly	Ile	His 70	Phe	Asp	Cys	Ser	Gly 75	Lys	Tyr	Arg	Cys 80	Arg	
Ser	Ser	Phe	Lys	Cys 85	Ile	Glu	Leu	Ile	Ala 90	Arg	Cys	Asp	Gly 95	Val	Ser	
Asp	Cys	Lys	Asp 100	Gly	Glu	Asp	Glu	Tyr 105	Arg	Cys	Val	Arg	Val 110	Gly	Gly	
Gln	Asn	Ala	Val	Leu	Gln	Val	Phe 120	Thr	Ala	Ala	Ser	Trp 125	Lys	Thr	Met	
Cys 130	Ser	Asp	Asp	Trp	Lys	Gly 135	His	Tyr	Ala	Asn	Val 140	Ala	Cys	Ala	Gln	
Leu 145	Gly	Phe	Pro	Ser	Tyr	Val 150	Ser	Ser	Asp	Asn	Leu	Arg	Val 160	Ser	Ser	
Leu	Glu	Gly	Gln	Phe 165	Arg	Glu	Glu	Phe	Val 170	Ser	Ile	Asp	His 175	Leu	Leu	
Pro	Asp	Asp	Lys 180	Val	Thr	Ala	Leu	His 185	His	Ser	Val	Tyr	Val 190	Arg	Glu	
Gly	Cys	Ala	Ser	Gly	His	Val	Val	Thr 200	Leu	Gln	Cys	Thr 205	Ala	Cys	Gly	
His 210	Arg	Arg	Gly	Tyr	Ser	Ser	Arg	Ile 215	Val	Gly	Gly 220	Asn	Met	Ser	Leu	
Leu 225	Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe 235	Gln	Gly	Tyr	His	
Leu	Cys	Gly	Gly	Ser 245	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr 255	Ala	Ala	
His	Cys	Val	Tyr	Asp 260	Leu	Tyr	Leu	Pro 265	Lys	Ser	Trp	Thr	Ile 270	Gln	Val	
Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn 280	Pro	Ala	Pro	Ser	His 285	Leu	Val	Glu	
Lys 290	Ile	Val	Tyr	His	Ser	Lys 295	Tyr	Lys	Pro	Lys	Arg	Leu	Gly	Asn	Asp	
Ile 305	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr	Phe 315	Asn	Glu	Met	Ile	
Gln	Pro	Val	Cys	Leu 325	Pro	Asn	Ser	Glu	Glu	Asn	Phe	Pro	Asp	Gly 335	Lys	
Val	Cys	Trp	Thr 340	Ser	Gly	Trp	Gly	Ala	Thr	Glu	Asp	Gly	Gly	Asp	Ala	

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<210> 3
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<212> DNA
<213> Homo sapiens
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<210> 4
<211> 260
<212> PRT
<213> Artificial Sequence
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 1             5             10             15
Gln Val Ser Leu Gln Val Arg Ser Gly Gly Gly Ser Arg Lys His Phe

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 Cys Gly Gly Ser Leu Ile Ser Glu Asn Trp Val Leu Thr Ala Ala His
 35 40 45
 Cys Val Ser Gly Ala Ala Ser Ala Pro Ala Ser Ser Val Arg Val Ser
 50 55 60
 Leu Ser Arg Val Arg Leu Gly Glu His Asn Leu Ser Leu Thr Glu Gly
 65 70 75 80
 Thr Glu Gln Lys Phe Asp Val Lys Lys Thr Ile Ile Val His Pro Asn
 85 90 95
 Tyr Asn Pro Asp Thr Leu Asp Asn Gly Ala Tyr Asp Asn Asp Ile Ala
 100 105 110
 Leu Leu Lys Leu Lys Ser Pro Gly Val Thr Leu Gly Asp Thr Val Arg
 115 120 125
 Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp Leu Pro Val Gly Thr Thr
 130 135 140
 Cys Thr Val Ser Gly Trp Gly Arg Arg Pro Thr Lys Asn Leu Gly Leu
 145 150 155 160
 Ser Asp Thr Leu Gln Glu Val Val Val Pro Val Val Ser Arg Glu Thr
 165 170 175
 Cys Arg Ser Ala Tyr Glu Tyr Gly Gly Thr Asp Asp Lys Val Glu Phe
 180 185 190
 Val Thr Asp Asn Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala
 195 200 205
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Asn Arg
 210 215 220
 Asp Gly Arg Trp Glu Leu Val Gly Ile Val Ser Trp Gly Ser Tyr Gly
 225 230 235 240
 Cys Ala Arg Gly Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser Tyr
 245 250 255
 Leu Asp Trp Ile
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<210> 5
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

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 Arg Ile Val Gly Gly Ser Glu Ala Lys Ile Gly Ser Phe Pro Trp Gln
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 20 25 30
 Thr Ala Ala His Cys Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 35 40 45
 Gly Glu Glu Thr Glu Gly Gly Pro Arg Leu Asp Ser Pro Gly Gly Gln
 50 55 60
 Val Ile Lys Val Ser Lys Ile Ile Glu Val His Pro Asn Tyr Asn Asn
 65 70 75 80
 Asp Ile Ala Leu Leu Lys Leu Lys Glu Pro Val Thr Leu Ser Asp Ser
 85 90 95
 Asn Thr Val Arg Pro Ile Cys Leu Pro Ser Ser Asn Glu Ile Lys Thr
 100 105 110
 Ser Glu Gly Asn Thr Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125

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Gly	Ser	Lys	Trp	Gly	Thr	Val	Cys	Asp	Ser	Ser	Trp	Ser	Leu	Arg	Asp
			20					25					30		
Ala	Asn	Val	Asp	Pro	Gln	Ala	Ser	Lys	Val	Cys	Arg	Gln	Leu	Gly	Cys
		35					40					45			
Gly	Gly	Ala	Val	Ser	Leu	Leu	Gly	Pro	Tyr	Phe	Ser	Glu	Gly	Gly	Gly
	50					55				60					
Pro	Ala	Gly	Gln	Arg	Glu	Ile	Trp	Leu	Asp	Gly	Val	Asn	Cys	Ser	Gly
65					70				75					80	
Asn	Glu	Thr	Ser	Leu	Ser	Gln	Cys	Pro	Val	Arg	Val	Thr	Pro	Pro	Gly
				85					90					95	
Leu	Ser	Arg	Gln	Cys	Ser	His	Asp	Gly	Glu	Asp	Ala	Gly	Val	Val	Cys
			100					105					110		
Ser															

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<400> 8
Arg Ile Val Gly Gly
  1               5
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<220>
<223> motif

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<221> VARIANT
<222> 5
<223> Xaa = Gly or Ser
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```
<400> 9
Gly Xaa Ser Gly Xaa
 1                      5
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<220>
<223> motif

```
<221> VARIANT
<222> 1
<223> Xaa = Leu, Ile, Val, or Met
```

```
<221> VARIANT
<222> 2
<223> Xaa = Ser or Thr
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```
<221> VARIANT
<222> 4
<223> Xaa = Ser, Thr, Ala, or Gly
```

```
<400> 10
Xaa Xaa Ala Xaa His Cys
  1                5
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```
<210> 11
<211> 2951
<212> DNA
<213> Homo sapiens
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[illegible]

gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gtg agt tca 1086

Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr	Val	Ser	Ser		
140						145			150								
gat	aac	ctc	aga	gtg	agc	tcg	ctg	gag	ggg	cag	ttc	cgg	gag	gag	ttt	1134	
Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe	Arg	Glu	Glu	Phe		
155						160			165								
gtg	tcc	atc	gat	cac	ctc	ttg	cca	gat	gac	aag	gtg	act	gca	tta	cac	1182	
Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys	Val	Thr	Ala	Leu	His		
170						175			180							185	
cac	tca	gta	tat	gtg	agg	gag	gga	tgt	gcc	tct	ggc	cac	gtg	gtt	acc	1230	
His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala	Ser	Gly	His	Val	Val	Thr		
			190						195			200					
ttg	cag	tgc	aca	gcc	tgt	ggg	cat	aga	agg	ggc	tac	agc	tca	cgc	atc	1278	
Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg	Arg	Gly	Tyr	Ser	Ser	Arg	Ile		
			205			210			215								
gtg	ggg	gga	aac	atg	tcc	ttg	ctc	tcg	cag	tgg	ccc	tgg	cag	gcc	agc	1326	
Val	Gly	Gly	Asn	Met	Ser	Leu	Leu	Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser		
			220			225			230								
ctt	cag	ttc	cag	ggc	tac	cac	ctg	tgc	ggg	ggc	tct	gtc	atc	acg	ccc	1374	
Leu	Gln	Phe	Gln	Gly	Tyr	His	Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro		
235						240			245								
ctg	tgg	atc	atc	act	gct	gca	cac	tgt	gtt	tat	gac	ttg	tac	ctc	ccc	1422	
Leu	Trp	Ile	Ile	Thr	Ala	Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro		
250			255			260			265								
aag	tca	tgg	acc	atc	cag	gtg	ggg	cta	gtt	tcc	ctg	ttg	gac	aat	cca	1470	
Lys	Ser	Trp	Thr	Ile	Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro		
			270			275			280								
gcc	cca	tcc	cac	ttg	gtg	gag	aag	att	gtc	tac	cac	agc	aag	tac	aag	1518	
Ala	Pro	Ser	His	Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys		
			285			290			295								
cca	aag	agg	ctg	ggc	aat	gac	atc	gcc	ctt	atg	aag	ctg	gcc	ggg	cca	1566	
Pro	Lys	Arg	Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro		
300			305			310			315								
ctc	acg	ttc	aat	gaa	atg	atc	cag	cct	gtg	tgc	ctg	ccc	aac	tct	gaa	1614	
Leu	Thr	Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu		
315			320			325			330								
gag	aac	ttc	ccc	gat	gga	aaa	gtg	tgc	tgg	acg	tca	gga	tgg	ggg	gcc	1662	
Glu	Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala		
330			335			340			345								
aca	gag	gat	gga	gca	ggg	gac	gcc	tcc	cct	gtc	ctg	aac	cac	gcg	gcc	1710	
Thr	Glu	Asp	Gly	Ala	Gly	Asp	Ala	Ser	Pro	Val	Leu	Asn	His	Ala	Ala		
			350			355			360								
gtc	cct	ttg	att	tcc	aac	aag	atc	tgc	aac	cac	agg	gac	gtg	tac	ggg	1758	
Val	Pro	Leu	Ile	Ser	Asn	Lys	Ile	Cys	Asn	His	Arg	Asp	Val	Tyr	Gly		

365	370	375	
ggc atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc			1806
Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly			
380	385	390	
gtg gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag			1854
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu			
395	400	405	
agg agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc			1902
Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys			
410	415	420	425
gca gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg			1950
Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu			
430	435	440	
gac tgg atc cac gag cag atg gag aga gac cta aaa acc tgaagaggaa			1999
Asp Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr			
445	450		
ggggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac			2059
tcccgtgtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt			2119
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